

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2003, 05:36:29 ; Search time 1275 seconds  
(without alignments)  
7315.604 Million cell updates/sec

Title: US-10-054-399A-1

Perfect score: 228

Sequence: 1 cccctctgtatacttttcaa.....aaacgctaataatccagc 228

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

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4: gb\_om.\*

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19: em\_mu.\*

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26: em\_to.\*

27: em\_sts.\*

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30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pin.\*

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36: em\_htg\_mam.\*

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38: em\_sy.\*

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40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID        | Description         |
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| 1          | 228   | 100.0 | 228    | 6  | AX004383  | AX004383 Sequence   |
| 2          | 228   | 100.0 | 228    | 6  | BD078523  | BD078523 Yeast Cdc  |
| 3          | 228   | 100.0 | 228    | 6  | E61227    | E61227 Nucleotide   |
| 4          | 226.4 | 99.3  | 228    | 6  | AX004385  | AX004385 Sequence   |
| 5          | 226.4 | 99.3  | 228    | 6  | AX004387  | AX004387 Sequence   |
| 6          | 226.4 | 99.3  | 228    | 6  | AX004389  | AX004389 Sequence   |
| 7          | 226.4 | 99.3  | 228    | 6  | BD078524  | BD078524 Yeast Cdc  |
| 8          | 226.4 | 99.3  | 228    | 6  | BD078525  | BD078525 Yeast Cdc  |
| 9          | 226.4 | 99.3  | 228    | 6  | BD078526  | BD078526 Yeast Cdc  |
| 10         | 226.4 | 99.3  | 228    | 6  | E61228    | E61228 Nucleotide   |
| 11         | 226.4 | 99.3  | 228    | 6  | E61229    | E61229 Nucleotide   |
| 12         | 226.4 | 99.3  | 228    | 6  | E61230    | E61230 Nucleotide   |
| 13         | 224.8 | 98.6  | 2000   | 6  | AX594660  | AX594660 Sequence   |
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| 15         | 224.8 | 98.6  | 103682 | 8  | SCUI2980  | U12980 Saccharomyc  |
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| 17         | 105.6 | 46.3  | 3908   | 8  | AF210636  | AF210636 Erethothec |
| 18         | 78.8  | 34.6  | 5915   | 8  | AY208122  | AY208122 Candida a  |
| 19         | 77.2  | 33.9  | 2535   | 6  | AX488842  | AX488842 Sequence   |
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| 22         | 42.8  | 18.8  | 37301  | 8  | SPAC1658  | 298529 S.pombe chr  |
| 23         | 41    | 18.0  | 138668 | 8  | AC092749  | AC092749 Genomic s  |
| 24         | 41    | 18.0  | 300029 | 8  | AE017081  | AE017081 Oryza sat  |
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| 33         | 38    | 16.7  | 2410   | 9  | L32611    | L32611 Homo sapien  |
| 34         | 38    | 16.7  | 2457   | 9  | HUM4PRO   | L03532 Human M4 pr  |
| 35         | 38    | 16.7  | 2514   | 9  | BC000138  | BC000138 Homo sapi  |
| 36         | 38    | 16.7  | 2542   | 9  | BC019580  | BC019580 Homo sapi  |
| 37         | 38    | 16.7  | 18889  | 9  | AL513476  | AL513476 Human DNA  |
| 38         | 38    | 16.7  | 74932  | 9  | AC008762  | AC008762 Homo sapi  |
| 39         | 38    | 16.7  | 147180 | 9  | AC136469  | AC136469 Homo sapi  |
| 40         | 38    | 16.7  | 156942 | 2  | AC136470  | AC136470 Homo sapi  |
| 41         | 37.8  | 16.6  | 186574 | 2  | AC123827  | AC123827 Mus muscu  |
| 42         | 37.6  | 16.5  | 2453   | 9  | AF061832  | AF061832 Homo sapi  |
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ALIGNMENTS

|             |            |   |        |     |        |                 |
|-------------|------------|---|--------|-----|--------|-----------------|
| RESULT 1    | AX004383   | Sequence 1 from Patent WO9918213.                                   | 228 bp | DNA | linear | PAT 24-AUG-2000 |
| AX004383    | LOCUS      | Sequence 1 from Patent WO9918213.                                   |        |     |        |                 |
| AX004383    | DEFINITION | Sequence 1 from Patent WO9918213.                                   |        |     |        |                 |
| AX004383    | ACCESSION  | Sequence 1 from Patent WO9918213.                                   |        |     |        |                 |
| AX004383..1 | VERSION    | GI:9927860  |        |     |        |                 |
| AX004383..1 | KEYWORDS   |   |        |     |        |                 |
| AX004383..1 | SOURCE     | synthetic construct   |        |     |        |                 |
| AX004383..1 | ORGANISM   | synthetic construct   |        |     |        |                 |
| AX004383..1 | REFERENCE  | artificial sequences.   |        |     |        |                 |
| AX004383..1 | AUTHORS    | Nern, P.M. and Arkowitz, R.A.                                       |        |     |        |                 |
| AX004383..1 | TITLE      | Mutants of yeast cdc24p, defective in binding of the g-protein beta |        |     |        |                 |
| AX004383..1 | JOURNAL    | subunit   |        |     |        |                 |
| AX004383..1 |            | Patent: WO 9918213-A 1 15-APR-1999;                                 |        |     |        |                 |

Pred. No. is the number of results predicted by chance to have a

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Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS      E61227      228 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Nucleotide sequence and protein sequence.
ACCESSION E61227
VERSION    E61227.1 GI:13027197
KEYWORDS   JP 1999113578-A/1.
SOURCE     unidentified
           unclassified.
REFERENCE   1 (bases 1 to 228)
AUTHORS    Robert A.A. and Pater, M.A.N.
TITLE       Nucleotide sequence and protein sequence
JOURNAL     Patent: JP 1999113578-A 1 27-APR-1999;
            MEDICAL RESEARCH COUNCIL
COMMENT     OS Unidentified
            PN JP 1999113578-A/1
            PD 27-APR-1999
            PF 21-OCT-1997 JP 1997326899
            PR 08-OCT-1997 GB 9721358.1
            PI ROBERT ALAN AKOVITSU,PETER MICHAEL ARUYOSHA NERUN PC
            CI2N15/09,A61K38/00,A61K38/00,C07K14/395//C07K14/82,G01N33/15, PC
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RESULT 2
BD078523
LOCUS      BD078523      228 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.
ACCESSION BD078523
VERSION    BD078523.1 GI:22624126
KEYWORDS   JP 2001519158-A/1.
SOURCE     synthetic construct
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           artificial sequences.
REFERENCE   1 (bases 1 to 228)
AUTHORS    Arkowitz, R.A. and Nern, P.M.A.
TITLE       Yeast Cdc24p variant lacking G protein beta-subunit bond
JOURNAL     Patent: JP 2001519158-A 1 23-OCT-2001;
            MEDICAL RESEARCH COUNCIL
COMMENT     OS Artificial Sequence
            PN JP 2001519158-A/1
            PD 23-OCT-2001
            PF 08-OCT-1998 JP 2000515009
            PR 08-OCT-1997 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR
            PI ROBERT ALAN ARKOWITZ,PETER MICHAEL ALJOSCHA NERN PC
            CI2N15/09,A61K38/00,A61K45/00,A61P43/00,C07K14/82,C12Q1/68, PC
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LOCUS AX004385 228 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 3 from Patent WO9918213.
ACCESSION AX004385
VERSION AX004385.1 GI:9927861
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Nern,P.M. and Arkowitz,R.A.
AUTHORS Mutants of yeast cdc24p, defective in binding of the g-protein beta
TITLE subunit
JOURNAL Patent: WO 9918213-A 3 15-APR-1999;
MEDICAL RES COUNCIL (GB); NERN PETER MICHAEL ALJOSCHA (GB)
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RESULT 5
AX004387
LOCUS AX004387 228 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 5 from Patent WO9918213.
ACCESSION AX004387
VERSION AX004387.1 GI:9927862
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Nern,P.M. and Arkowitz,R.A.
AUTHORS Mutants of yeast cdc24p, defective in binding of the g-protein beta
TITLE subunit
JOURNAL Patent: WO 9918213-A 5 15-APR-1999;
MEDICAL RES COUNCIL (GB); NERN PETER MICHAEL ALJOSCHA (GB)
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LOCUS AX004389 228 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 7 from Patent WO9918213.
ACCESSION AX004389
VERSION AX004389.1 GI:9927863
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Nern,P.M. and Arkowitz,R.A.
AUTHORS Mutants of yeast cdc24p, defective in binding of the g-protein beta
TITLE subunit
JOURNAL Patent: WO 9918213-A 7 15-APR-1999;
MEDICAL RES COUNCIL (GB); NERN PETER MICHAEL ALJOSCHA (GB)
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LOCUS BD078524 228 bp DNA linear PAT 27-AUG-2002
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.
ACCESSION BD078524
VERSION BD078524.1 GI:22624127
KEYWORDS JP 2001519158-A/2.
SOURCE synthetic construct
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ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 228)  
REFERENCE Arkowitz,R.A. and Nern,P.M.A.  
AUTHORS Yeast Cdc24p variant lacking G protein beta-subunit bond  
TITLE Patent: JP 2001519158-A 2 23-OCT-2001;  
JOURNAL MEDICAL RESEARCH COUNCIL  
COMMENT OS Artificial Sequence  
PN JP 2001519158-A/2  
PD 23-OCT-2001  
PF 08-OCT-1998 JP 2000515009  
PR 08-OCT-1997 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR  
12-JUN-1998 GB 9812793.9  
PI ROBERT ALAN ARKOWITZ,PETER MICHAEL ALJOSCHA NERN PC  
C12N15/09,A61K38/00,A61K45/00,C07K14/82,C12Q1/68, PC  
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DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.  
ACCESSION BD078525  
VERSION BD078525.1 GI:22624128  
KEYWORDS JP 2001519158-A/3.  
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ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 228)  
REFERENCE Arkowitz,R.A. and Nern,P.M.A.  
AUTHORS Yeast Cdc24p variant lacking G protein beta-subunit bond  
TITLE Patent: JP 2001519158-A 3 23-OCT-2001;  
JOURNAL MEDICAL RESEARCH COUNCIL  
COMMENT OS Artificial Sequence  
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PD 23-OCT-2001  
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12-JUN-1998 GB 9812793.9  
PI ROBERT ALAN ARKOWITZ,PETER MICHAEL ALJOSCHA NERN PC  
C12N15/09,A61K38/00,A61K45/00,A61P43/00,C07K14/82,C12Q1/68, PC  
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PC C12N15/00,A61K37/02  
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QY 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGCCAACTCGACGTC 180  
DB 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGCCAACTCGACGTC 180  
QY 181 CAGCTGTCGAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
DB 181 CAGCTGTCGAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
RESULT 9  
BD078526  
LOCUS 228 bp DNA linear PAT 27-AUG-2002  
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.  
ACCESSION BD078526  
VERSION BD078526.1 GI:22624129  
KEYWORDS JP 2001519158-A/4.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 228)  
REFERENCE Arkowitz,R.A. and Nern,P.M.A.  
AUTHORS Yeast Cdc24p variant lacking G protein beta-subunit bond  
TITLE Patent: JP 2001519158-A 4 23-OCT-2001;  
JOURNAL MEDICAL RESEARCH COUNCIL  
COMMENT OS Artificial Sequence  
PN JP 2001519158-A/4  
PD 23-OCT-2001  
PF 08-OCT-1998 JP 2000515009  
PR 08-OCT-1997 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR  
12-JUN-1998 GB 9812793.9  
PI ROBERT ALAN ARKOWITZ,PETER MICHAEL ALJOSCHA NERN PC  
C12N15/09,A61K38/00,A61K45/00,A61P43/00,C07K14/82,C12Q1/68, PC  
G01N33/566,  
PC C12N15/00,A61K37/02  
CC Description of Artificial Sequence: nucleic acid FH Key  
FT Location/Qualifiers  
FT source 1..228  
/organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..228  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

G01N33/566,  
PC C12N15/00,A61K37/02  
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FT Location/Qualifiers  
FT source 1..228  
/organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..228  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
BASE COUNT 67 a 49 c 43 g 69 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCCCTCTGTATACITTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAATAGCATCT 60  
DB 1 CCCCTCTGTATACITTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAATAGCATCT 60  
QY 61 GACGATTGGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAAACAC 120  
DB 61 GCGGATTGGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAAACAC 120  
QY 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGCCAACTCGACGTC 180  
DB 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGCCAACTCGACGTC 180  
QY 181 CAGCTGTCGAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
DB 181 CAGCTGTCGAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
RESULT 9  
BD078526  
LOCUS 228 bp DNA linear PAT 27-AUG-2002  
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.  
ACCESSION BD078526  
VERSION BD078526.1 GI:22624129  
KEYWORDS JP 2001519158-A/4.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 228)  
REFERENCE Arkowitz,R.A. and Nern,P.M.A.  
AUTHORS Yeast Cdc24p variant lacking G protein beta-subunit bond  
TITLE Patent: JP 2001519158-A 4 23-OCT-2001;  
JOURNAL MEDICAL RESEARCH COUNCIL  
COMMENT OS Artificial Sequence  
PN JP 2001519158-A/4  
PD 23-OCT-2001  
PF 08-OCT-1998 JP 2000515009  
PR 08-OCT-1997 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR  
12-JUN-1998 GB 9812793.9  
PI ROBERT ALAN ARKOWITZ,PETER MICHAEL ALJOSCHA NERN PC  
C12N15/09,A61K38/00,A61K45/00,A61P43/00,C07K14/82,C12Q1/68, PC  
G01N33/566,  
PC C12N15/00,A61K37/02  
CC Description of Artificial Sequence: nucleic acid FH Key  
FT Location/Qualifiers  
FT source 1..228  
/organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..228  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
BASE COUNT 68 a 50 c 42 g 68 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCCCTCTGTATACITTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAATAGCATCT 60  
DB 1 CCCCTCTGTATACITTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAATAGCATTT 60  
QY 61 GACGATTGGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAAACAC 120  
DB 61 GCGGATTGGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAAACAC 120  
QY 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGCCAACTCGACGTC 180  
DB 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGCCAACTCGACGTC 180  
QY 181 CAGCTGTCGAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
DB 181 CAGCTGTCGAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
RESULT 9  
BD078526  
LOCUS 228 bp DNA linear PAT 27-AUG-2002  
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.  
ACCESSION BD078526  
VERSION BD078526.1 GI:22624129  
KEYWORDS JP 2001519158-A/4.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 228)  
REFERENCE Arkowitz,R.A. and Nern,P.M.A.  
AUTHORS Yeast Cdc24p variant lacking G protein beta-subunit bond  
TITLE Patent: JP 2001519158-A 4 23-OCT-2001;  
JOURNAL MEDICAL RESEARCH COUNCIL  
COMMENT OS Artificial Sequence  
PN JP 2001519158-A/4  
PD 23-OCT-2001  
PF 08-OCT-1998 JP 2000515009  
PR 08-OCT-1997 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR  
12-JUN-1998 GB 9812793.9  
PI ROBERT ALAN ARKOWITZ,PETER MICHAEL ALJOSCHA NERN PC  
C12N15/09,A61K38/00,A61K45/00,A61P43/00,C07K14/82,C12Q1/68, PC  
G01N33/566,  
PC C12N15/00,A61K37/02  
CC Description of Artificial Sequence: nucleic acid FH Key  
FT Location/Qualifiers  
FT source 1..228  
/organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..228  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

Best Local Similarity 99.6%; Pred. No. 2.3e-52;

Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAAATAGCATCT 60  
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Db 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAAATAGCACCT 60  
|||||

Qy 61 GACGATTTGAAGTCTGTAAAAATCCATTTATGACTTTATATTTGGCTGCAAGAACAC 120  
|||||

Db 61 GACGATTTGAAGTCTGTAAAAATCCATTTATGACTTTATATTTGGCTGCAAGAACAC 120  
|||||

Qy 121 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAAACCTCGACGTC 180  
|||||

Db 121 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAAACCTCGACGTC 180  
|||||

Qy 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||

Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
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RESULT 10  
E61228 LOCUS 228 bp DNA linear PAT 18-JUN-2001  
DEFINITION Nucleotide sequence and protein sequence.  
ACCESSION E61228  
VERSION F61228.1 GI:13027198  
KEYWORDS JP 1999113578-A/2.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 228)  
AUTHORS Robert,A.A. and Pater,M.A.N.  
TITLE Nucleotide sequence and protein sequence  
JOURNAL Patent: JP 1999113578-A 2 27-APR-1999;  
MEDICAL RESEARCH COUNCIL

COMMENT OS Unidentified  
PN JP 1999113578-A/2  
PD 27-APR-1999 JP 1997326899  
PF 21-OCT-1997 GB 9721358:1  
PR 08-OCT-1997 GB 9721358:1  
PI ROBERT ALAN AKOVITTSU,PATER MICHAEL ARUYOSHA NERUN PC  
C12N15/09,A61K31/70,A61K38/00,C07K14/395//C07K14/82,G01N33/15, PC  
C12N15/00,  
PC A61K37/02

CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..228 /organism='Unidentified'.  
FT

FEATURES  
source  
1..228  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

BASE COUNT 68 a 48 c 42 g 70 t

ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAAATAGCATCT 60  
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Db 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAAATAGCATTT 60  
|||||

Qy 61 GACGATTTGAAGTCTGTAAAAATCCATTTATGACTTTATATTTGGCTGCAAGAACAC 120  
|||||

Db 61 GACGATTTGAAGTCTGTAAAAATCCATTTATGACTTTATATTTGGCTGCAAGAACAC 120  
|||||

Qy 121 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAAACCTCGACGTC 180  
|||||

Db 121 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAAACCTCGACGTC 180  
|||||

Qy 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||

Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
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Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
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RESULT 11

E61229 LOCUS 228 bp DNA linear PAT 18-JUN-2001

DEFINITION Nucleotide sequence and protein sequence.

ACCESSION E61229

VERSION E61229.1 GI:13027199

KEYWORDS JP 1999113578-A/3.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 228)

AUTHORS Robert,A.A. and Pater,M.A.N.

TITLE Nucleotide sequence and protein sequence

JOURNAL Patent: JP 1999113578-A 3 27-APR-1999;  
MEDICAL RESEARCH COUNCIL

COMMENT OS Unidentified

PN JP 1999113578-A/3

PD 27-APR-1999

PF 21-OCT-1997 JP 1997326899

PR 08-OCT-1997 GB 9721358:1

PI ROBERT ALAN AKOVITTSU,PATER MICHAEL ARUYOSHA NERUN PC

C12N15/09,A61K31/70,A61K38/00,C07K14/395//C07K14/82,G01N33/15, PC

C12N15/00,  
PC A61K37/02

CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..228 /organism='Unidentified'.  
FT

FEATURES  
source  
1..228  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

BASE COUNT 67 a 49 c 43 g 69 t

ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAAATAGCATCT 60  
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Db 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAAATAGCATCT 60  
|||||

Qy 61 GACGATTTGAAGTCTGTAAAAATCCATTTATGACTTTATATTTGGCTGCAAGAACAC 120  
|||||

Db 61 GACGATTTGAAGTCTGTAAAAATCCATTTATGACTTTATATTTGGCTGCAAGAACAC 120  
|||||

Qy 121 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAAACCTCGACGTC 180  
|||||

Db 121 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAAACCTCGACGTC 180  
|||||

Qy 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||

Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||

RESULT 12

E61230 LOCUS 228 bp DNA linear PAT 18-JUN-2001

DEFINITION Nucleotide sequence and protein sequence.

ACCESSION E61230

VERSION E61230.1 GI:13027200

KEYWORDS JP 1999113578-A/4.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 228)

AUTHORS Robert,A.A. and Pater,M.A.N.

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TITLE      Nucleotide sequence and protein sequence
JOURNAL    Patent: JP 1999113578-A 4 27-APR-1999;
COMMENT    MEDICAL RESEARCH COUNCIL
OS         Unidentified
PN         JP 1999113578-A/4
PD         27-APR-1999
PR         21-OCT-1997 JP 1997326899
PF         08-OCT-1997 GB 9721358.1
PI         ROBERT ALAN AKOVITTSU, PATER MICHAEL ARUYOSHA NERUN PC
C12N15/09,A61K31/70,A61K38/00,C07K14/395//C07K14/82,G01N33/15. PC
C12N15/00;
CC         A61K37/02
PC         Topology: Linear;
FH         Key Location/Qualifiers
FT         source 1..228
            Location/Qualifiers
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
            68 a 50 c 42 g 68 t

BASE COUNT 68 a 50 c 42 g 68 t
ORIGIN
Query Match 99.34; Score 226.4; DB 6; Length 228;
Best Local Similarity 99.6%; Pred. No. 2.3e-52;
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGTATACCTTTCAACTCTGTGAAGCGCAATTTAAATACGGTAATAGCATCT 60
   |||||
DB 1 CCCCTGTATACCTTTCAACTCTGTGAAGCGCAATTTAAATACGGTAATAGCATCT 60
   |||||

QY 61 GACGATTGAAAGTCTGTAAAAATCCATTATGACCTTTATATGGGCTGCAAGAACAC 120
   |||||
DB 61 GACGATTGAAAGTCTGTAAAAATCCATTATGACCTTTATATGGGCTGCAAGAACAC 120
   |||||

QY 121 TTTCGATTAAAGTCTGTAAAAATCCATTATGACCTTTATATGGGCTGCAAGAACAC 180
   |||||
DB 121 TTTCGATTAAAGTCTGTAAAAATCCATTATGACCTTTATATGGGCTGCAAGAACAC 180
   |||||

QY 181 CAGCTGGTCAAGTCTGTAGAAGTAGTAGAAGCGTAATGAATCCAGC 228
   |||||
DB 181 CAGCTGGTCAAGTCTGTAGAAGTAGTAGAAGCGTAATGAATCCAGC 228
   |||||

RESULT 13
LOCUS      AX594660 2000 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 314 from Patent EP1258494.
ACCESSION  AX594660
VERSION     AX594660.1 GI:28396414
KEYWORDS    Saccharomyces cerevisiae (baker's yeast)
SOURCE      Saccharomyces cerevisiae
ORGANISM    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1
AUTHORS     Bauer A., Gavin A.C., Grandi P., Krause R., Kruse U., Kuester R.,
            Marzioch M., Schultz J. and Superti-Furga G.
TITLE       Multiprotein complexes from eukaryotes
JOURNAL     Patent: EP 1258494-A 314 20-NOV-2002;
            CELLZONE AG (DE)
FEATURES    Location/Qualifiers
            source 1..2000
            /organism="Saccharomyces cerevisiae"
            /mol_type="genomic DNA"
            /db_xref="taxon:4932"
            659 a 423 c 365 g 553 t

BASE COUNT 659 a 423 c 365 g 553 t
ORIGIN
Query Match 98.6%; Score 224.8; DB 6; Length 2020;
Best Local Similarity 99.1%; Pred. No. 6.6e-52;
Matches 226; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGTATACCTTTCAACTCTGTGAAGCGCAATTTAAATACGGTAATAGCATCT 60
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DB 1 CCCCTGTATACCTTTCAACTCTGTGAAGCGCAATTTAAATACGGTAATAGCATCT 60
   |||||

QY 61 GACGATTGAAAGTCTGTAAAAATCCATTATGACCTTTATATGGGCTGCAAGAACAC 120
   |||||
DB 61 GACGATTGAAAGTCTGTAAAAATCCATTATGACCTTTATATGGGCTGCAAGAACAC 120
   |||||

QY 121 TTTCGATTAAAGTCTGTAAAAATCCATTATGACCTTTATATGGGCTGCAAGAACAC 180
   |||||
DB 121 TTTCGATTAAAGTCTGTAAAAATCCATTATGACCTTTATATGGGCTGCAAGAACAC 180
   |||||

QY 181 CAGCTGGTCAAGTCTGTAGAAGTAGTAGAAGCGTAATGAATCCAGC 228
   |||||
DB 181 CAGCTGGTCAAGTCTGTAGAAGTAGTAGAAGCGTAATGAATCCAGC 228
   |||||

RESULT 14
LOCUS      YSCCL54A 2811 bp DNA linear PLN 04-DEC-1995
DEFINITION Yeast (S.cerevisiae) CLS4 gene encoding a Ca regulatory protein,
            complete cds.
ACCESSION  M16809
VERSION     M16809.1 GI:1100996
KEYWORDS    calcium regulatory protein.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
ORGANISM    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1
AUTHORS     Miyamoto S., Ohya Y., Sano Y., Sakaguchi S., Iida H. and Anraku Y.
TITLE       A DBL-homologous region of the yeast CLS4/CDC24 gene product is
            important for Ca(2+)-modulated bud assembly
JOURNAL     Biochem. Biophys. Res. Commun. 181 (2), 604-610 (1991)
MEDLINE     92095962
PUBMED      1755844
REFERENCE   2
AUTHORS     Miyamoto S., Ohya Y., Ohsumi Y. and Anraku Y.
TITLE       Nucleotide sequence of the CLS4 (CDC24) gene of Saccharomyces
            cerevisiae
JOURNAL     Gene 54 (1), 125-132 (1987)
MEDLINE     87277425
PUBMED      3301539
COMMENT     On Dec 4, 1995 this sequence version replaced gi:171246.
            Original source text: Yeast (S.cerevisiae strain YOC138-10A)) DNA,
            clone pFOM105.
FEATURES    Location/Qualifiers
            source 1..2811
            /organism="Saccharomyces cerevisiae"
            /mol_type="genomic DNA"
            /db_xref="taxon:4932"
            124..2688
            /note="Calcium regulatory protein"
            /codon_start=1
            /db_xref="GI:1100997"
            /translation="MAIQTFASGTSLDLKPKPSATSIIPMONVKNKPVTEQSLF
            HICANIRLEVLPLQKPFLOLAYQSSEVLSEKQSLLSQKHOELLKSNKARDSSD
            LAPTRSSISLSTMSMEGISTNSPSAIPNEDTLTFSMGLPITMDCDPVTQ
            LSQFGQAGPLCILFNSVKPQFLPVASDOLKVKKSIYDFILGCKHFAFNDSEELF
            TISDFEANSQLVKLEVTNNSSPTIFPSKSTQOIMNAENQHRHQPOQSKKH
            NFYVKIIRFVATERKYVHDLIDKYRQQLDSNLTISELYMFLPNLDAIDFORR
            FLISLEINALEVPSKQIRIGALFMHKKHFFKLYEPWSIGQNAAYIFLSLTKHKNVDS
            ORFIINNKLEQSLYKPVORLYPLVAKELLAESSDDNNTKEALSDISNIARS
            INENORRTENHQVKKLYGRVYVKNKGRYISKFGELLYFDKVFISTISSEPEREPEY
            YLFEXIILFSEVTKKSSALLIKSSSTASISNITDNNGSPHHSFHKRRNS
            SSNIHLSSSSAAAIHSTNSDNNSSSSSLFKLSANEPKLDURGIMLNQ
            IIPQNNRSINITWESIKEQGNFLFKRNEETRDNSMAFSSSHMKRVDVLPKRRHSS
            TSTTSKAKSSMSPTTMTPNHNSRQTHDSMAFSSSHMKRVDVLPKRRHSS
            SPSEIKSISENFKNIPESILPRIYSNNNSNTSSSEIFTLLVEKWNFDLIMAI
            NSKISNTNNNISPTIKKYQDEGDFVLGSDENNVAKEMLAENKEFLNRLY"

BASE COUNT 950 a 581 c 508 g 772 t

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ORIGIN 1 bp upstream of HindIII site.

Query Match 98.6%; Score 224.8; DB 8; Length 2811;  
Best Local Similarity 99.1%; Pred. No. 6.6e-52;  
Matches 226; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTCTGTATCTTTCAACTCTCTGAGCGCAATTAATACCGGTAAATAGCATCT 60  
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DB 631 CCCCTCTGTATCTTTCAACTCTCTGAGCGCAATTAATACCGGTAAATAGCATCT 690  
|||||  
QY 61 GACGATTTGAAAGTCTGTAATAAAATCCATTATGACTTTATATTGGGCTGCAAGAAACAC 120  
|||||  
DB 691 GACGATTTGAAAGTCTGTAATAAAATCCATTATGACTTTATATTGGGCTGCAAGAAACAC 750  
|||||  
QY 121 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGAGCTTTTGCACATCAGCTCC 180  
|||||  
DB 751 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGAGCTTTTGCACATCAGCTCC 810  
|||||  
QY 181 CAGCTGGTCAAAAGTCTGAGAACTAGTAGAAGCGTAATGAATTCACG 228  
|||||  
DB 811 CAGCTGGTCAAAAGTCTGAGAACTAGTAGAAGCGTAATGAATTCACG 858  
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RESULT 15

SCU12980  
LOCUS SCU12980 103682 bp DNA linear PLN 05-MAR-1998  
DEFINITION Saccharomyces cerevisiae chromosome I left arm sequence.  
ACCESSION U12980 U00091  
VERSION U12980.1 GI:2911250  
KEYWORDS S.cerevisiae Ycr28p homolog; FLO9; GOH3; two alcohol/sorbitol  
dehydrogenase homologs; SIM1; CNE1; ACS1; S.pombe SPAC1P7.03  
homolog; S.cerevisiae P1p2p-like transcription factor homolog;  
GCV3, glycine cleavage H protein; PTAL; FUN9 transcript, essential  
gene, S.pombe SPAC 24B11.08c homolog; CDC24; CLN3/WHI1/DAF2; CYC3;  
PYK1; S.cerevisiae ORF 06283 homolog; Xenopus laevis GTP-binding  
protein DRG homolog; FUN12 transcript, essential gene; FUN19  
transcript, S.cerevisiae orf 06265 homolog; FUN53 transcript,  
essential gene; FUN20 transcript, essential gene, S.pombe SPAC  
8A4.06 homolog; SNL1; MYO2; S.cerevisiae ORF 06159 homolog; DR52;  
MAK16; LTEL.

SOURCE Saccharomyces cerevisiae (baker's yeast)

ORGANISM Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE  
AUTHORS Nagasu,T. and Hall,B.D.  
TITLE Nucleotide sequence of the GDH gene coding for the NADP-specific  
glutamate dehydrogenase of Saccharomyces cerevisiae  
JOURNAL Gene 37 (1-3), 247-253 (1985)  
MEDLINE 86031359  
PUBMED 2932370

REFERENCE  
AUTHORS Dumont,M.E., Ernst,J.F., Hampsey,D.M. and Sherman,F.  
TITLE Identification and sequence of the gene encoding cytochrome c heme  
lyase in the yeast Saccharomyces cerevisiae  
EMBO J. 6 (1), 235-241 (1987)  
MEDLINE 87218469  
PUBMED 3034577

REFERENCE  
AUTHORS Miyamoto,S., Ohya,Y., Ohsumi,Y. and Anraku,Y.  
TITLE Nucleotide sequence of the CLS4 (CDC24) gene of Saccharomyces  
cerevisiae  
JOURNAL Gene 54 (1), 125-132 (1987)  
MEDLINE 87277425  
PUBMED 3101539

REFERENCE  
AUTHORS Wickner,R.B.  
TITLE Host function of MAK16: G1 arrest by a mak16 mutant of  
Saccharomyces cerevisiae  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6007-6011 (1988)  
MEDLINE 88320371  
PUBMED 3045810

REFERENCE  
AUTHORS

AUTHORS Nash,R., Tokiwa,G., Anand,S., Erickson,K. and Futcher,A.B.  
TITLE The WHI1+ gene of Saccharomyces cerevisiae tethers cell division to  
cell size and is a cyclin homolog  
JOURNAL EMBO J. 7 (13), 4335-4346 (1988)  
MEDLINE 89210821  
PUBMED 2907481  
REFERENCE 6 (sites)  
AUTHORS McNally,T., Purvis,I.J., Fothergill-Gilmore,L.A. and Brown,A.J.  
TITLE The yeast pyruvate kinase gene does not contain a string of  
non-preferred codons: revised nucleotide sequence  
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